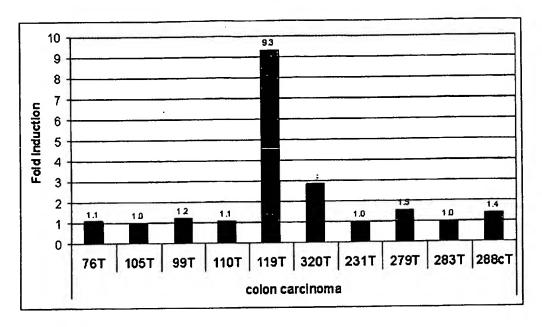
WO 03/089667 PCT/EP03/03827

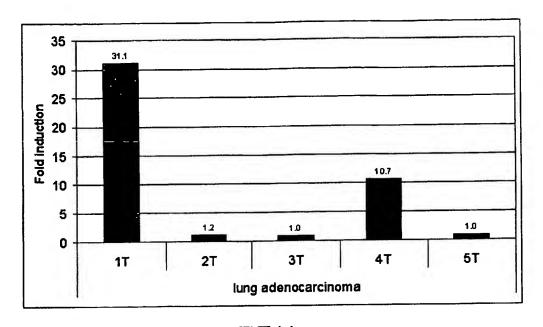
Figure 1:



TKT-L1

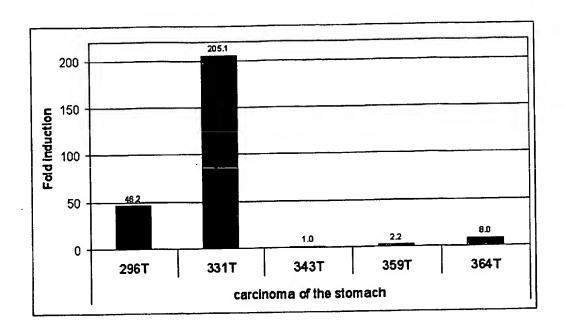
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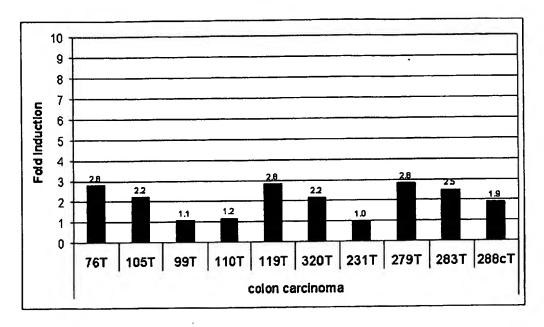
TKT-L1

Figure 3:



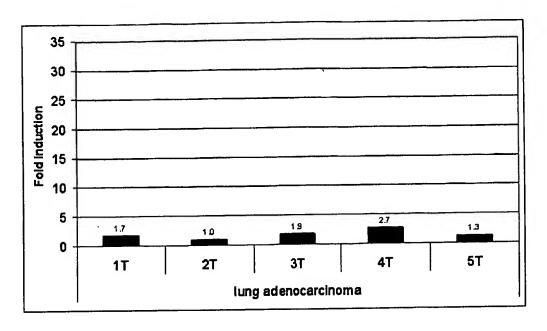
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Figure 4:



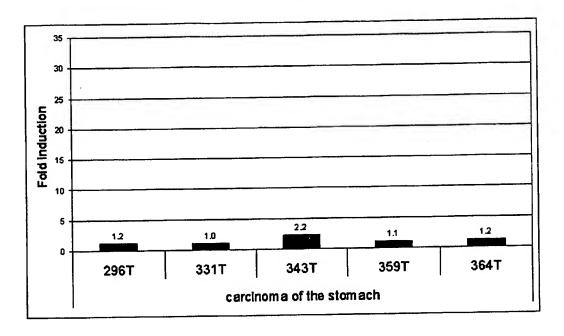
TKT

Figure 5:



TKT

Figure 6



TKT

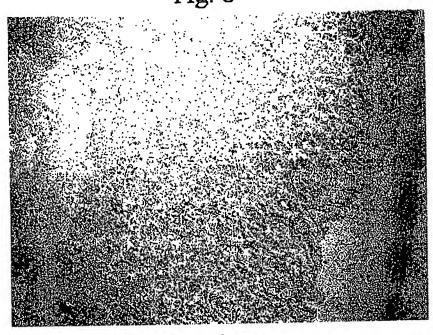
Fig. 7: DNA and amino acid sequence of TKT-L1

1	GCCAT	TCG	CT	CTT	CAG	ACG	CCG	GAG.	ACG	TAG	GAG	TGG	GTC'	TTC	AGA	CTC	CAA	AGG	GGT'	ľG
61	GACTA	አ ጥር	ימרנ	GA'	rgc'	TGA	GĠC(GAG	GGC'	TGA	GTT	ccc	GGA	GGA	GGC	CAG	ACC'	TGA.	CAG	GG
61	GHCIN	M	A	D	A	E	A	R	A	E	F	P	E	Ε	A	R	P	D	R	G
121	GCACC	TTO	GCA(GGT(GTT	GCA	AGA'	TAT	GGC	CAG	CCG	CTT	GCG	AAT	CCA	TTC	CAT	CAG	GGC	CA
	T	L	Q	V	L	Q	D	M	A	S	R	L	R	Ι	H	S	I	R	A	T
181	CATGC	TC	CAC	GAG	CTC	CGG	CCA	CCC	TAC	ATC	ATG	TAG	CAG	TTC	TTC	TGA	GAT	CAT	GTC'	TG
	С	S	T	S	S	G	H	P	Т	S	С	S	S	S	S	E	1	М	S	٧
241	TGCTG	TT	CTT	CTA	CAT	CAT	GAG	GTA	CAA	GCA	GTC	AGA	TCC	AGA	GAA	īcc	GGA	CAA	CGA	CC
	_	F													N					
301	GATTT	GT(CCT	CGC	AAA	GAG	ACT	GTC	GTT	TGT	GGA	TGT	GGC	AAC	AGG	ATG	GCT	CGG	ACA	AG
	F	V	L	Α	K	R	ь	Ş	F.	V	ע	V	А	1	G	74	п	G	¥	G
361	GACTG	GGZ	AGT'	TGC	ATG	TGG	AAT	GGC	ATA	TAC	TGG	CAA	GTA	CTI	'CGA	CAG	GGC	CAG	CTA	CC
001	L	G	V	A	C	G	M	Α	Y	T	G	K	Y	F	D	R	A	S	Y	R
	GGGTG			~~~	~~ m	~~~	max	maa	M/13	OT C	יטייט	מיי מי	אכיכי	CTC	יייביי	ירידים	രവ	ממת	דממ	GG
421	GGGTG	TT(CTG	CCT	CAT	GAG S	TGA	G	E	S	S	AGA E	и G	S	v	W	E	A	М	A
481	CCTTT	GC:	rtc	CTA	CTA	CAG	TCT	GGA	CAA	TÇI	TGT	GGC	TAA	'CTI	TGA	TGT	GAA N	DDD.	CCT	GG
															D					
541	GACAC	AG:	TGG	TGC	ATT	GCC	CGC	CGA	.GCA	CTG	CAT	AAA	CAT	CTA	TCA	GAG	GCG	CIG	CGA	AG
	H	8	G	A	L	P	A	R	H	C	7	N	1	I	Q	K	v	•	_	•
601	CCTTI	:GG	GTG	GAA	CAC	TTA	TGT	GGI	'GGA	CGG	CCG	GGA	CGI	'GG7	.GGC	ACT	GTG	CCA	GGT	ΆŢ
601		G	W	N	T	¥	V	V	D	G	R	D	V	E	A	L	С	Q	V	F
601 661	CCTTI F TCTGG	G	₩ ccc	anic.	T TCA	Y CCT	V	V .GCA	D	G	R CAC	D TGC:	V TG1	e GGI	A rggo	L :CAA	C .GAC	Q CTI	V CAA	.GG
	F	G	₩ ccc	anic.	T TCA	Y CCT	V	V .GCA	D	G	R CAC	D TGC:	V TG1	e GGI	A	L :CAA	C .GAC	Q CTI	V CAA	.GG
661	TCTGG	G CA Q	W GGC A CAC	TTC S	T TCA Q PAAG	Y .GGT V :TAT	V GAA K TGA	V .GCA H .GGA	D .CAA K .TGC	G GCC P :AGA	R CAC T	D TGC A	V TG1 V	E GGI V	A TGGC A CAAA	L CAA K AGCC	C GAC T	Q CTI F	V CAA K :GAG	GG G G
	TCTGG	G CA Q	W GGC A CAC	TTC S	T TCA Q PAAG	Y .GGT V :TAT	V GAA K TGA	V .GCA H .GGA	D .CAA K .TGC	G GCC P :AGA	R CAC T	D TGC A	V TG1 V	E GGI V	A TGGC A	L CAA K AGCC	C GAC T	Q CTI F	V CAA K :GAG	GG G G
661 721	TCTGG W GCCGG R	G SCA Q SGG G	W GGC A CAC	TTC S CCC	TCA Q AAG	Y .GGT V TAT	V GAA K TGA	V GCA H .GGA	D CAA K TGC A	G GCC P P AGI	R CAC T LAAG B	D TGC A TTC	V TGI V GCA	E 'GGT V LTGC A	A TGGC A ZAAA K	L CAA K AGCC	GAC T 'AAT M	CTT F	CAA K GAG	GG G RAG E
661	TCTGG	G SCA Q SGG G	W GGC A CAC	N TTC 8 CCC P	TCA Q AAG S	Y .GGT V TAT I	V GAA K TGA	V GCA H .GGA D	D CAA K TGC A	G GCC P AGI E	R CAC T LAAG B	D TGC A TTC W	V TGT V GCA H	E 'GGT V LTGC A	A TGGC A ZAAA K	CAA K AGCC P	GAC T AAT M	CTI F CCC P	CAA K GAG R	GG G RAG E
661 721	TCTGG W GCCGG R AAAGA	G Q Q G G AGC.	W GGC A CAC T AGA D	TTC S CCCC P TGC	TCA Q AAG S CAT	Y GGT V TAT I	V GAA K TGA E CAA K	GCA H GGA D ATT	D CAA K TGC A CAAT	G GCC P AGA E TGA	R CAC T LAAG B LGAG	TGC A TTGC W TTG W	V TGT V GCA H	E GGT V TGC A	A TGGC A CAAA K AGAC T	CAA K AGCC P CAG	GAC T AAT M CAC	CTT F GCC P GAM	CAA K GAG R TCT	GG G AG E
661 721	TCTGG	G G Q G G A A C	W GGC A CAC T AGA D	TTC 8 CCC P TGC A	TCA Q AAG S CAT	Y GGT V TAT I	V GAA K TGA E CAA K	V GCA H GGA D ATT	D CAA K TGC A CAAT	G GCC P AGI E TGI	R CAC T LAAG B LGAG B	D TGC A TTG W CCA	V TGT V GCA H GAT I	E GGI V TGC A TAC!	A TGGC A CAAA K AGAC T	CAA K AGCC P CAG	GAC T AAT M CAG R	CTT F GCC P GAA	CAA K GAG R TCT L	GG G G AG E T D
661 721 781	TCTGG W GCCGG R AAAGA ACCCA	G Q G G A A A C A	GGC A CAC T AGA D GCC	TTC 8 CCC P TGC A	TCA Q PAAG S CAT I	GGT V TAT I TAT I	V GAA K TGA E CAA K GGA	V GCA H GGA D ATT L	D CAA K TGC A CAAT I	G P AGA E TGA E	R CAC T LAAC B LAGA S LAGI	TGC A STTC W SCCA	V TGT V GCA H GAT I	E V TGC A TAC!	A CAAA K AGAC T	CAA K AGCC P CAG E ATGT V	GAC T AAT M SCAG R	GCC P GGAR GAR GAR M	CAA K GAG R TCT L	GG G AG E TG D
661 721 781	TCTGG W GCCGG R AAAGA ACCCA	G G G G G A A CA	W GGC A CAC T AGA D GCC	TTC S CCCC P A CCCC	TCA Q AAG SCAT ICAT	Y CGT V TAT I TAT I TGA	V GAA TGA TGA K CAA K GGA	V GCA H GGA D ATT L GTC	CAATI CACC	G GCC P AGA E TGA E TGA	R CAC T LAAG B LGAG B LAGI	TGC A TTGC W CCA CCA TTGC TAGC	V TGT V GCA H GAT I	E V TGC A TCAC T	A CAGA	CAAAAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GAC TAAT M CAC R	GAN GAN GAN GAN GAN	CAA K GAG R TCT L CGAC	GG G G E T G G G G G G G G G G G G G G G
661 721 781 841	TCTGG W GCCGG R AAAGA ACCCA	G GCA Q GGG G AGC A	W GGC A CAC T AGA D GCC	TTC S CCCC P A CCCC	TCA Q AAG SCAT ICAT	Y CGT V TAT I TAT I TGA	V GAA TGA TGA K CAA K GGA	V GCA H GGA D ATT L GTC	CAATI CACC	G GCC P AGA E TGA E TGA	R CAC T LAAG B LGAG B LAGI	TGC A TTGC W CCA CCA TTGC TAGC	V TGT V GCA H GAT I	E V TGC A TCAC T	A CAAA K AGAC T	CAAAAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GAC TAAT M CAC R	GAN GAN GAN GAN GAN	CAA K GAG R TCT L CGAC	GG G G E T G G G G G G G G G G G G G G G
661 721 781 841 901	TCTGG R GCCGG R AAAGA R ACCCA P CTCCA	G GCA Q GGG AGC ACA ACA P	W GGC A CAC T AGA D GCC P TGA	TTCC P TGCC P TTTA	T TCA Q AAAG S CAT I CAG R	Y GGT V TAT I TAT I TAGA E AGGT	V GAAA K TGAA E CAAA K GGAA GGAA GGAA GGAA GGAA GGAA	V GGA H GGA D ATTI L GTG B	D CAME K TGC A I I I I I I I I I I I I I I I I I I	G AGCO P LAGIA E TTGI E AGAT I LAGIA	R CCAC T LAAC B LAGAC S LAGAC S LAGAC A LAGC LAGC LAGC LAGC LAGC LAGC L	D TTGG A W GCCA CCAA TTGG	V V V V V GGCA H LGAT I LCAT I TTCC R	E GGGI V ATGC A TACI TACI T GGAI K GGAI	A PGGGGA R R AGAC T CAGA AAAG AAAG AAAG AAAG AAAG AA	L CCAA K AGCC P CCAG S ATGT V CATGG	GACACACACACACACACACACACACACACACACACACAC	Q CCTT F CGCC P CGCAN M CGAN M L CCAN CCAN CCAN CCAN CCAN CCAN CCAN CC	CCAA K CGAG R TCT TCGAC T	GG G G EAG E T G D C T G G G G G G G G G G G G G G G G G G
661 721 781 841	TCTGG R GCCGG R AAAGA R ACCCA P CTCCA	G GCA Q GGG AGC ACA ACA P	W GGC A CAC T AGA D GCC P TGA	TTCC P TGCC P TTTA	T TCA Q AAAG S CAT I CAG R	Y GGT V TAT I TAT I TAGA E AGGT	V GAAA K TGAA E CAAA K GGAA GGAA GGAA GGAA GGAA GGAA	V GGA H GGA D ATTI L GTG B	D CAME K TGC A I I I I I I I I I I I I I I I I I I	G AGCO P EAGN E TTGN E AGAT I EAGAT	R CCAC T LAAC B LAGAC S LAGAC S LAGAC A LAGC LAGC LAGC LAGC LAGC LAGC L	D TTGG A W GCCA CCAA TTGG	V V V V V GGCA H LGAT I LCAT I TTCC R	E GGGI V ATGC A TACI TACI T GGAI K GGAI	A PGGGGA R R AGAC T CAGA AAAG AAAG AAAG AAAG AAAG AA	L CCAA K AGCC P CCAG S ATGT V CATGG	GACACACACACACACACACACACACACACACACACACAC	Q CCTT F CGCC P CGCAN M CGAN M L CCAN CCAN CCAN CCAN CCAN CCAN CCAN CC	CCAA K CGAG R TCT TCGAC T	GG G G EAG E T G D C T G G G G G G G G G G G G G G G G G G
661 721 781 841 901	TCTGG R GCCGG R AAAGA R ACCCA P CTCCA P	G GGG G G A A CA P TAA K	W GGCC T AGA D GCCC P TGA D GCCT L	N TTC S CCC P TGC A CCCC P	T TCA Q AAG S CAT I CAG R CAG R	Y GGT V TTAT I TTAT I TGA E GAGT V ACGC	CAAA K CAAAA K CAAAAA K CAAAA K CAAAAA K CAAAAAA K CAAAAA K CAAAAAAA K CAAAAAAAA	V GGA H GGA D ATT L GTG B CTGA D ACAM	D CAA K ATGC A CAAT I CAC P ACAA K ACAC R	G AGCO P EAGI	R CCAC T LAAG B LGAG B LAGG V LAGG V V CCGT	D A A A A A C C C A A C C C A A C C C A A C	V V GGCA H AGAT I ACAT I TTCC R	E CGGI	A CAGACA T D A A A A A A A A A A A A A A A A A	L CAA K AGCCO P CCAG B ATGT V CATGG C	GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Q CCTT F CGCC P CGAN M CGAN M	CAAA K GAG R TCT L CGAC T	GGG G G E E E E E E E E E E E E E E E E
661 721 781 841 901	TCTGG W GCCGG R AAAGA ACCCA P CTCCA A CTCCA	G GGGG G A A A CA P TAA K	W GGC A CAC T AGA D GCC T TGA C C C C C C C C C C C C C C C C C C C	N TTC S CCC P TGC A CCCC P TGC G CCCC CCC CCC CCC CCC CCC CCC CCC	T TCA Q RAAG S CAT I CAG R CAG R	Y GGT V TAT I TAT I TGA E AGT V	V GAA K TGAA E CAA K GGA TGG G	V GCA H GCA D L CTC 8 CTC C B L CTC A CTC	D CAA K K TGC A I LACC P LCAA R A CGG	G GCC P FAGA E E GCC E E GCC E E GCC	R CCAC T LAAGE B LAGAGE V LAGCO V ACCC	D A A A A A A C C C A A C C A A C C A A C C C A A C	V V GGCA H AGATI CTCC R AGCCA L AGCCA	E GGGT V A TGC A A TGC A T GGGA K GGGA T D GGGT T GGGGT T GGGGT T GGGGT T GGGGT T GGGT	A CAST	CCAAA CCAGCO P CCAGG B ATGT V CCAGG CCAGG B ATGT CCAGG	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Q F F GGCC P GGAN M GGAN M CCAC R	CAAA K GAGG R L L CGAC T CGGC A A GGTA	GG G EAG E TTG D CT L CT B STG B
661 721 781 841 901 961	TCTGGGRAM GCCGGRAM AAAGAA ACCCA P CTCCA A CTACCA T	G GCA Q GGG G A ACC P TAA K	W GGC A CAC T AGA D GCC P TGA C CTC 8	N TTC S CCC P TGC A CCCC P TTA Y CGGG G TTGA	T TCA Q AAG 8 CAT I CAG R CAG R CAG R	Y GGT V TAT I TGA E AGT V ACGC A TATI	V GAA K TGAA K GGAA CGAA CGAA CGAA CGAA	GCA ATTI	CAATACAATACAACAACAACAACAACAACAACAACAACAA	G AGCO P AGA E TTGA E TTGA E AGA I AGA Y	R R CCAC T IAAG B AGAG B IAGAG B IAGAG P	D TGC A TTGC W CCAA TTGT TTGT CTGF	V GCA H AGAT I ACAT R FIGCT L AGCC R	E GGGI V ATGC A FACI Q CCAC T GGGAI K CGGGI F GGGAI F F GGGT F	A CAAAA K LAGAC T CAAAA A CC A A CC C C C C C C C C C	CCAA AGCC P CCAG S ATGT V CATG C C CTGA C C C C C C C C C C C C C C C C C C C	GAC T AAT M GCAG R TAAG R GCGG G G	Q GCTT F GCC P GGAN GGAN M GCTC R GCTN F	CAAA K CGAG R T CGGC A GGTA M	GG G G E E E E E E E E E E E E E E E E
661 721 781 841 901 961	TCTGGGRANGER R AAAGAR R ACCCAR P CTCCAR TCTGGGTT	G GCA Q GGG G A A CA A CC P TAA K	W GGC A CAC T AGA D GCC P TGA C CTC 8	TTCC P TGC A CCCC P TGC A CCCC P TGC CCCC CCC CCC CCCC CCCC CCCC	T TCA Q PAAG S CAT I CAG	GGTTAT I TAT I TGA E ACGC A TATI	GAAA E CAAA G D C CAAA C C C C C C C C C C C C C C C	V GCA H GCA L CTC S CTC	D CAM R LTGC A LTGC A LCAL R R LCAL R R LCAL R R R R R R R R R R R R R R R R R R R	G GCC P FAGA E E TTGA E TTGA I LAGATA Y TTGGG	R R CCAC T IAAG B AGAG B AGAG C T CGT ACCC P	D TGC A TTGC W GCCA TTGC TTGC TTGC TTGC E TTGC E TTGC TTGC	V TGT V GGA H LGAT I TGCT R AGCCT	E GGGI V ATGC A FACA PACA T GGGA K FGGA FGGA FGGA FGGA FGGA FGGA FG	A CAGA T CAGA A CAGA C C C C C C C C C C C C C C	L CAAA AGCC P CCAG B ATGT V CATGA C C CTGA C C C C C C C C C C C C C C C C C C C	GAC T PART M SCAG TAAG TAAG G G CAC C C C C C C C C C C C C C C C C C C	Q CTT F GCC P GGAN M GGAN M GCC R GC	CAAA K GAG R TTCT L CGGC A GGTA M TTGC	GG G GAG E TG D CT L CT L CT A CTT
661 721 781 841 901 961	TCTGGGRANGER R AAAGAR R ACCCAR P CTCCAR TCTGGGTT	G GCA Q GGG G A A CA A CC P TAA K	W GGC A CAC T AGA D GCC P TGA C CTC 8	TTCC P TGC A CCCC P TGC A CCCC P TGC CCCC CCC CCC CCCC CCCC CCCC	T TCA Q PAAG S CAT I CAG	GGTTAT I TAT I TGA E ACGC A TATI	GAAA E CAAA G D C CAAA C C C C C C C C C C C C C C C	V GCA H GCA L CTC S CTC	D CAM R LTGC A LTGC A LCAL R R LCAL R LCAL R R LCAL R R R R R R R R R R R R R R R R R R R	G GCC P FAGA E E TTGA E TTGA E TTGA TA GATA Y TTGGG	R R CCAC T IAAG B AGAG B AGAG C T CGT ACCC P	D TGC A TTGC W GCCA TTGC TTGC TTGC TTGC E TTGC E TTGC TTGC	V TGI V GGA H LGAI I TGCI R LGCI R CCI CCI CCI CCI CCI CCI CCI CCI CCI	E GGGI V ATGC A FACA PACA T GGGA K FGGA FGGA FGGA FGGA FGGA FGGA FG	A CAAAA K LAGAC T CAAAA A CC A A CC C C C C C C C C C	L CAAA AGCC P CCAG B ATGT V CATGA C C CTGA C C C C C C C C C C C C C C C C C C C	GAC T PART M SCAG TAAG TAAG G G CAC C C C C C C C C C C C C C C C C C C	Q CTT F GCC P GGAN M GGAN M GCC R GC	CAAA K GAG R TTCT L CGGC A GGTA M TTGC	GG G GAG E TG D CT L CT L CT A CTT
661 721 781 841 901 961	TCTGGGRAAAGAAAGAAAGAAAGAAAGAAAAGAAAAGAAA	G GCAGG G G AGC. A CA P TAA K TTT F A CA	GGC AGA D GCC P GCT B AAAA N GCA C	TTC S CCCC P TGC A CCCC P TTA Y CGGG C TGA A CCCC M	T TCA S S S S S S S S S S S S S S S S S S S	GGTT V TATT I TTAT I TTGA E AGT V AGG A TATT F TGAG 8	GAAA E CAAA C C C C C C C C C C C C C C C	V GCA H GGA D ATTI	CAAATI CA	G G G G G G G G G G G G G G G G G G G	R CCAC T LAAG B LAGG S LAGG V LAGG V LAGG C C C C C C C C C C C C C C C C C C	D TGC A TGC W CCAM TT TGT V TTGT E TTGT A CATT	V TGT V GGCA H AGATI ACATI TGCT R TGCT R TGCT R TGCT R	E GGG V V TGC A TGC A TGG B K TGG B F CC CC R A TGG B	A CAGACA T CAGACA T CAGACA T CAGACA A CAGACA T CAGACA A CAGACA T C	CCAAA AGCC P CCAG ATGT V CATGT C CTGF E AGCC R CTGF R TCGF R TCGF	GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GCTT F GCCT P GGAN GGAN GGAN GGAN GGAN GGAN GGAN GG	CAAA K GAGA R T T T T T T T T T T T T T T T T T T	GG G GAG E TTG D CT B CT L L CT B CT F F GC C

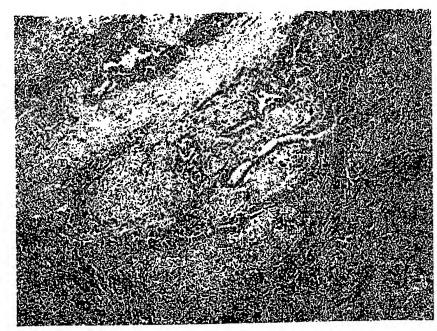
PCT/EP03/03827

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1261	GTGC	rtc S	CCA Q	GAT(M	GGC(A	CCT(L	GGA E	GGA' D	TAT.	AGC A	CAT M	GTT F	CCG. R	AAC T	CAT I	TCC(CAA K	GTG C	CAC	GA I
1321	TCTT		CCC.	AAC'. T	rga: D	rgc(A	CGT V	CTC S	CAC T	GGA E	GCA H	TGC A	TGT V	TGC A	TCT L	GGC A	AGC A	CAA' N	TGC(A	CA K
1381	AGGG			CTT(F		rcg(R	GAC T	CAC T	CCG R	ACC P	AGA E	AAC T	TAT M	GGT V	TAT I	TTA Y	CAC T	CCC. P	ACA: Q	AG E
1441	AACG R		TGA E	GAT I	CGG;	ACA(Q	GGC A	CAA K	GGT V	CCT L	CCG R	CCA H	CTG C	TGT V	CAG S	TGA D	CAA K	GGT V	CAC.	AG V
1501	TTAT			TGG: G		TAC'	TGT V	GTA Y	TGA E	AGC A	CTT L	AGC A	AGC A	TGC A	TGA D	TGA E	GCT L	TTC S	GAA. K	AC Q
1561	AAGA D	TAT I	_	TAT	CCG R	TGT V	CAT I	CGA D	CCT L	GTI F	TAC T	CAT	TAA K	ACC P	TCT L	'GGA D	TGT V	CGC A	CAC T	CA
1621	TCGT V		CAG S	TGC.	AAA K	AGC A	CAC T	AGA E	.GGG	CCG R	GAT I	CAT	TAC T	AGT V	GGA E	.GGA D	TCA H	CTA Y	P P	GC Q
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1741	ATTC	GCI	rggc A	AGT V	GTC S	GGG. G	AGT V	GCC P	CCA Q	GAC S	TGG G	GAA K	GTC S	CGA E	GGA E	ATT L	GCT L	GGA D	TAT. M	'GT Y
1801	ATGG G	AAI I	DATT S	TGC A	CAG R	ACA H	TAT I	CAT	AGT V	GG(CGT V	GAA K	ATG C	CAI M	GTT L	GCT L	GAA N	CTA *	AAA	ΑTA
1861	GCTG	TT	AGCC	TTG	GTC	TTT	TGG	CCI	'CTT	'TAC	CCT	GTG	TTT	'ATC	TTT	GTT	'CCA	AAA	CCA	TC
1921	ATTT	'AA	ATCI	CTA	.CTG	TCA	CAT	TTI	'GT'I	TCI	TAP	AAG	CAA	AGC	CAC	CTA	ACA	CCT	'TCA	TT
1981	CATC	CC1	ragi	TCG	GAA	TTA	CAA	GCI	'AAC	TA(TT	CCC	TTT	'AAF	CTG	TCA	CTG	CAT	ATG	CA
2041	AGTA	CCC	3CTC	TAA	TTT	TTG	GAI	'CAT	'TAP	AGC	GAG	STTA	CAC	'AAC	TTI	'TAA	GTG	AAA	AAA	TA
2101	AGGI	'AA'	CAAA	ACA	ACC	ACC	TGA	TAG	TAF	GT	TTC	TGF	TAF	GAC	TAT	(AGA	AAT!	GTG	GTA	\GA
2161	GGTA	TA/	CAAI	TCT	TCC	GAA	GTG	TTI	CCI	TC	TG!	ATA	ACI	'GG'	'AGI	\GGI	'AA'	'AGI	TTT:	TT
2221	CAAT	GT	ATTI	CCI	TCA	TGA	GTA	AAC	AA	ATO	STG	TAE	'GA	AGT?	ATA	TTAE	:CCA	IGTA	\GCC	TA
2281	GTTI	CC	ACAG	CAC	'GAT	'AAC	ACC	ATC	ACC	CC:	[AC]	rgc1	GTI	ccc	CACC	TTC	€G₽	YTTC	TG1	GT
2341	GCTG	SC C	ATCO	CAC	CTG	CAG	CTO	CCC	TGO	'AA	rtc(CTI	CGC	TG	TTT	3CC1	TCF	\TCI	rccc	CTC
2401	CACC	TT:	TGAG	AGG	CTG	TCA	GGC	AGO	CAGO	CGA	AAG(CTTC	TT?	\GGI	ATGI	rcci	GTG	3CTG	3CTI	GI
2461	GATO	DAE	AGCO	CTCC	ACA	CTG	TAC	TG	TC	AAG?	rca/	ATGI	ATT	ATA	AAG	TAC	TC!	\AA/	4CCF	AAA
2521	AAA	AA	AAA	A.A																

Fig. 8

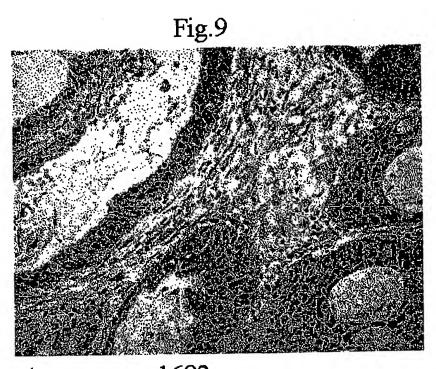


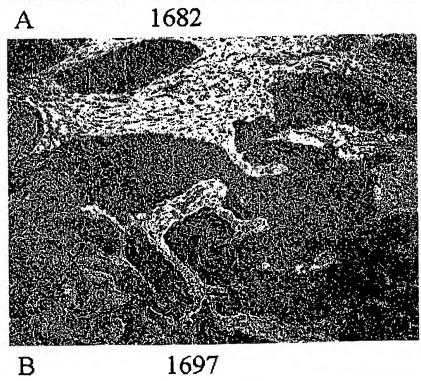
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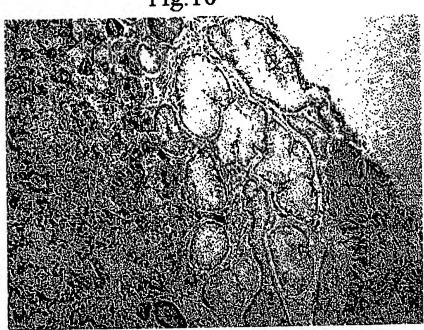
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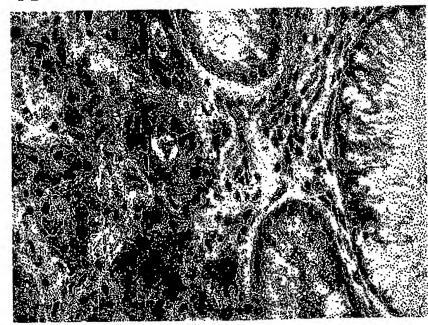




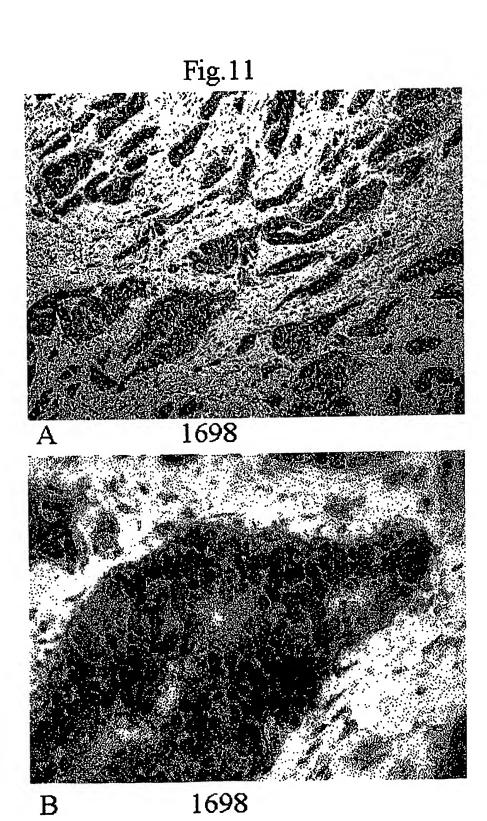








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